Patent claims

1. A homoserine transsuccinylase which possesses at least one mutation as compared with a homoserine transsuccinylase wild-type enzyme and exhibits a reduced sensitivity toward L-methionine or SAM as compared with the wild-type enzyme, with the wild-type enzyme possessing an amino acid sequence which comprises a constituent sequence AspGlyXaaXaaXaaThrGlyAlaPro between positions 90 and 115 and a constituent sequence TyrGlnXaaThrPro between positions 285 and 310, with position 1 of the amino acid sequence being the starting methionine, characterized in that the mutation is an amino acid replacement of the aspartate in the constituent sequence AspGlyXaaXaaXaaThrGlyAlaPro or an amino acid replacement of the tyrosine in the constituent sequence TyrGlnXaaThrPro.

2. A homoserine transsuccinylase as claimed in claim 1, characterized in that it exhibits a resistance toward SAM or L-methionine which is increased (increased Ki) at least 2-fold as compared with that of the wild type.

3. A homoserine transsuccinylase as claimed in claim 1 or 2, characterized in that it contains one of the mutations listed in Table 1.

4. A metA allele which encodes a homoserine transsuccinylase as claimed in one of claims 1 to 3.

5. A plasmid, characterized in that it contains a metA allele as claimed in claim 4 together with a promoter.

6. A microorganism strain, characterized in that it contains a feedback-resistant metA allele as claimed in claim 4.

7. A microorganism strain as claimed in claim 6, characterized in that it is a Gram-negative bacterial strain, preferably E. coli.

8. A method for preparing L-methionine or SAM by culturing a microorganism strain as claimed in claim 6 or 7.